

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:53:22 ; Search time 29 Seconds
(without alignments)
362.196 Million cell updates/sec

Title: US-09-997-585-399

Perfect score: 656
Sequence: 1 MLPPALPPALVFTVAMSLA.....SAQLLCMPVGARGALCQ 120

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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172	60.5	9.2	522	US-10-026-106E-8	Sequence 8, Appl1	245	59	9.0	261	US-08-927-219-55	Sequence 55, Appl

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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:53:37 ; Search time 40 Seconds
(without alignments)
288.650 Million cell updates/sec

Title: US-09-997-585-399
Sequence: 1 MLPPALPPALVFTVANSLLA.....SAQLCCPVGVARGALCO 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : PIR 80.*
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2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	# Match	Length	DB	ID	Description
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3	76.5	11.7	113	2	A34792	Ig heavy chain pre
4	76	11.6	1133	2	A54164	sterol regulatory
5	75.5	11.5	368	2	T44887	probable branched-
6	74.5	11.4	835	2	T06590	probable beta-gala
7	73	11.1	224	2	A13021	two component reep
8	73	11.1	244	2	A98263	transcription regu
9	72.5	11.1	3104	2	S20473	fatty-acid synthas
10	72	11.0	159	2	B83245	hypothetical prote
11	72	11.0	1063	2	A40253	acidic nuclear pro
12	71.5	10.9	236	2	T36188	hypothetical prote
13	71	10.8	210	2	B75450	hypothetical prote
14	71	10.8	342	2	AD0346	probable transport
15	70.5	10.7	368	2	C70786	probable live prot
16	70.5	10.7	456	2	T06136	aspartate transami
17	70.5	10.7	591	2	F83472	probable glycosyl
18	70	10.7	321	2	AB1054	probable membrane
19	70	10.7	478	2	C87351	aldehyde dehydroge
20	69.5	10.6	345	2	T35357	hypothetical prote
21	69.5	10.6	418	2	S46315	aspartate transami
22	69.5	10.6	535	2	F70782	probable transami
23	69	10.5	392	2	T35487	hypothetical prote
24	69	10.5	893	2	H95953	probable difunctio
25	69	10.5	1234	2	AB4310	cobalamin biosynth
26	68.5	10.4	140	2	S54240	Ig mu heavy chain
27	68	10.4	581	2	G70189	threonine-trna lig
28	68	10.4	592	2	D70863	hypothetical prote
29	67.5	10.3	312	2	C75377	probable glucose 6

30	67.5	10.3	420	2	T08005	flavonol 3-O-glucos
31	67	10.2	264	2	E72642	hypothetical prote
32	67	10.2	1381	2	T31083	parandrin - rat
33	67	10.2	1385	2	T14158	neurixin IV - mous
34	66.5	10.1	115	2	S19665	Ig heavy chain V r
35	66.5	10.1	355	2	C85552	phosphoribosylamln
36	66.5	10.1	355	2	AB90701	phosphoribosylamln
37	66.5	10.1	1019	2	AB2136	polyketide synthas
38	66.5	10.1	1154	2	S43275	hypothetical prote
39	66.5	10.1	1339	2	T47841	hypothetical prote
40	66	10.1	154	2	AB0176	methylyglyoxal synt
41	66	10.1	218	2	H70856	hypothetical prote
42	65.5	10.0	101	2	E72698	hypothetical prote
43	65.5	10.0	201	2	T07729	wound-induced prote
44	65.5	10.0	231	2	S77323	hypothetical prote
45	65.5	10.0	235	2	AB0114	deoxyribonuclease
46	65.5	10.0	266	1	TLBP2X	tall fiber protein
47	65.5	10.0	304	2	T37060	hypothetical prote
48	65.5	10.0	427	2	JC4915	age protein precur
49	65.5	10.0	466	2	B70932	probable PPS prote
50	65.5	10.0	1827	2	B70984	probable polyketid
51	65	9.9	352	2	A25466	photoactive II pro
52	65	9.9	357	2	T33507	hypothetical prote
53	65	9.9	368	2	G86416	hypothetical prote
54	65	9.9	2090	2	T30075	hypothetical prote
55	65	9.9	2153	2	T30074	hypothetical prote
56	64.5	9.8	238	2	D95984	conserved hypotnet
57	64.5	9.8	424	2	S09884	hypothetical prote
58	64.5	9.8	883	1	OYBC	phosphoenolpyruvat
59	64.5	9.8	883	2	B86087	phosphoenolpyruvat
60	64.5	9.8	883	2	E91239	phosphoenolpyruvat
61	64.5	9.8	883	2	S42136	phosphoenolpyruvat
62	64	9.8	1748	2	Q01740	cnjB protein - Tet
63	64	9.8	120	2	Q01740	hypothetical 12.7k
64	64	9.8	260	1	JS0635	rRNA (adenine-N6-)
65	64	9.8	564	2	H86278	phosphoenolpyruvat
66	64	9.8	619	2	A45625	probable aldehyde
67	64	9.8	746	2	F95890	glycogen phosphory
68	64	9.8	847	1	A25518	genomic polypeptin
69	64	9.8	2183	1	GANNB4	hepatic lectin H1
70	63.5	9.7	291	1	LNHJ1	phosphoribosylamln
71	63.5	9.7	355	2	DCEBPK	aspartate transami
72	63.5	9.7	449	2	T48511	probable fructuron
73	63.5	9.7	486	2	A64909	probable oxidoredu
74	63.5	9.7	486	2	H85719	probable oxidoredu
75	63.5	9.7	618	2	T49741	related to stress
76	63	9.6	233	2	JC7618	FRAT2 protein - hu
77	63	9.6	395	2	G69373	glutaryl-CoA dehyd
78	63	9.6	475	2	S49886	probable membrane
79	63	9.6	488	2	T19884	hypothetical prote
80	62.5	9.5	190	1	A44593	endo-1,4-beta-xyls
81	62.5	9.5	318	2	G84143	hypothetical prote
82	62.5	9.5	476	1	JC2318	angiotensin precur
83	62.5	9.5	561	2	D84800	hypothetical prote
84	62.5	9.5	628	2	D90677	probable propionyl
85	62.5	9.5	628	2	C85527	probable propionyl
86	62.5	9.5	746	2	T35811	probable phosphodi
87	62.5	9.5	883	2	AD0936	phosphoenolpyruvat
88	62.5	9.5	1442	2	T42607	transcription acti
89	62	9.5	140	2	AE3007	conserved hypotnet
90	62	9.5	160	2	A96277	hypothetical prote
91	62	9.5	160	2	AC2799	conserved hypotnet
92	62	9.5	280	2	I48713	phox2 homeodomain
93	62	9.5	382	2	G70946	probable dioxysens
94	62	9.5	402	2	T52356	related to GTP-bin
95	62	9.5	706	2	F86143	hypothetical prote
96	62	9.5	766	2	A75332	probable DNA misme
97	62	9.5	1321	2	T00382	hypothetical prote
98	62	9.5	3670	2	T36249	CNA peptide synthe
99	61.5	9.4	212	2	T49680	related to immedi
100	61.5	9.4	288	1	P3VXFS	3a protein - psenu
101	61.5	9.4	337	2	T52358	probable CELL DIVI
102	61.5	9.4	398	2	A36926	aspartyl proteinas

103	61.5	9.4	407	2	JC5124	aspartate transami
104	61.5	9.4	426	2	B71408	probable acylamino
105	61.5	9.4	441	2	A83170	probable MFS trans
106	61.5	9.4	764	2	JC8016	acylaminoacyl-pept
107	61.5	9.4	1417	2	H83132	probable sensor/re
108	61.5	9.4	3461	2	S58870	treelin precursor
109	61	9.3	115	2	T51208	hypothetical prote
110	61	9.3	260	2	S49386	capsid protein V2
111	61	9.3	312	2	C75561	conserved hypochat
112	61	9.3	435	2	AF2079	hypothetical prote
113	61	9.3	540	2	AD0522	probable exported
114	61	9.3	570	1	A45591	hemagglutinin prec
115	61	9.3	614	2	A25707	UI snRNP 70K prote
116	61	9.3	632	2	C86922	probable membrane
117	61	9.3	850	2	S22338	glycogen phosphory
118	61	9.3	2706	2	T28155	variant-specific s
119	60.5	9.2	209	2	JC4909	endo-1,4-beta-xylo
120	60.5	9.2	235	2	AE0877	endonuclease I [lm
121	60.5	9.2	261	1	WM8XE	infected cell prot
122	60.5	9.2	342	2	H86336	hypothetical prote
123	60.5	9.2	346	2	H85057	probable transposo
124	60.5	9.2	438	2	B70779	probable kasb prot
125	60.5	9.2	487	2	S61243	deoxyribonuclease
126	60.5	9.2	509	2	JC5055	high affinity nitr
127	60.5	9.2	529	2	G83442	probable 3-hydroxy
128	60.5	9.2	572	2	T34658	hypothetical prote
129	60.5	9.2	572	2	AF3068	two component sens
130	60.5	9.2	579	2	E98218	exeg protein (A)22
131	60.5	9.2	643	2	H64119	chrooine-cRNA 11g
132	60.5	9.2	825	2	H64083	bicoin sulfoxide r
133	60.5	9.2	935	2	E96806	hypothetical prote
134	60.5	9.2	1230	2	E64664	outer membrane pro
135	60.5	9.2	1237	2	D71850	probable outer mem
136	60	9.1	80	2	E83102	conserved hypochet
137	60	9.1	135	2	T01322	aluminum-induced p
138	60	9.1	257	2	A43362	env polyprotein -
139	60	9.1	283	2	C83248	hypothetical prote
140	60	9.1	378	2	AF3320	flavohemoprotein l
141	60	9.1	381	2	G70626	hypothetical prote
142	60	9.1	398	2	G82755	conserved hypochet
143	60	9.1	410	2	T36610	hypothetical prote
144	60	9.1	484	2	B70586	probable amia2 pro
145	60	9.1	504	2	A84244	probable signaling
146	60	9.1	563	1	HMTVCV	hemagglutinin prec
147	60	9.1	672	1	S73438	MG032 homolog B01
148	60	9.1	789	1	Q08EE3	HMLF1 protein - hu
149	60	9.1	819	2	B87386	hypothetical prote
150	60	9.1	846	1	Q08EC3	HORF1 protein - hu
151	60	9.1	947	2	H85088	hypothetical prote
152	60	9.1	1007	2	H72734	hypothetical prote
153	60	9.1	1487	1	EDBBE1	immediate-early pr
154	60	9.1	1487	1	EDBBE6	155K transcripion
155	59.5	9.1	122	2	S30533	Ig heavy chain V r
156	59.5	9.1	168	2	C70824	probable transcrip
157	59.5	9.1	190	1	A44594	endo-1,4-beta-xylo
158	59.5	9.1	213	1	A44594	endo-1,4-beta-xylo
159	59.5	9.1	213	1	A40569	endo-1,4-beta-xylo
160	59.5	9.1	213	1	S01734	endo-1,4-beta-xylo
161	59.5	9.1	213	1	S48126	endo-1,4-beta-xylo
162	59.5	9.1	222	2	S39154	xylanase 1 - fungu
163	59.5	9.1	223	2	S39883	endo-1,4-beta-xylo
164	59.5	9.1	223	2	T16335	hypothetical prote
165	59.5	9.1	333	2	T39642	conserved hypochet
166	59.5	9.1	392	2	T01849	hypothetical prote
167	59.5	9.1	395	2	D81729	Mt/TnaB/TyO perm
168	59.5	9.1	405	2	T14311	aspartate transami
169	59.5	9.1	409	2	S53303	aspartate transami
170	59.5	9.1	412	1	XNCHDC	aspartate transami
171	59.5	9.1	413	1	XNPDGC	aspartate transami
172	59.5	9.1	503	2	H95390	probable reverse t
173	59.5	9.1	553	2	AH3191	canase (imported)
174	59.5	9.1	564	2	AH2066	hypothetical prote
175	59.5	9.1	570	2	T20166	hypothetical prote
176	59.5	9.1	646	2	D82492	conserved hypochet
177	59.5	9.1	954	1	S20907	endo-1,4-beta-xylo
178	59.5	9.1	959	2	E85276	hypothetical prote
179	59.5	9.1	1376	2	F72609	probable reverse g
180	59.5	9.1	2610	2	T20968	hypothetical prote
181	59.5	9.1	123	2	A36006	Ig heavy chain V r
182	59	9.0	238	2	A80006	tRNA nucleotidyltr
183	59	9.0	241	2	S53522	crystalin beta B1
184	59	9.0	260	1	VCCWV	coat protein - whe
185	59	9.0	296	2	A87000	probable chloisula
186	59	9.0	307	2	F71294	hypothetical prote
187	59	9.0	365	2	A47045	cobalt/zinc/cadmiu
188	59	9.0	369	2	C85497	probable fibribrial
189	59	9.0	369	2	C90646	probable fibribrial
190	59	9.0	413	2	S01076	aspartate transami
191	59	9.0	477	2	H70747	probable ammonium
192	59	9.0	479	2	G82114	sigma-54 dependent
193	59	9.0	485	2	G71239	hypothetical prote
194	59	9.0	538	2	T40992	hypothetical prote
195	59	9.0	570	2	S22013	hemagglutinin prec
196	59	9.0	570	2	S22017	hemagglutinin prec
197	59	9.0	672	2	T36083	pyruvate, phosphat
198	59	9.0	953	2	S56650	pyruvate, phosphat
199	59	9.0	953	2	S12894	hypothetical prote
200	59	9.0	1075	2	T48805	probable RNA-dirc
201	59	9.0	1309	2	T00078	hypothetical prote
202	59	9.0	1677	2	T14267	Xin protein, stage
203	59	9.0	1897	1	TDHULK	leukocyte antigen-
204	58.5	8.9	120	2	B72519	hypothetical prote
205	58.5	8.9	210	2	C83762	endo-1,4-beta-xylo
206	58.5	8.9	248	2	AE1040	conserved hypochet
207	58.5	8.9	248	2	S56531	hypothetical 27.4k
208	58.5	8.9	321	2	B87658	hypothetical prote
209	58.5	8.9	342	2	S14432	heterogeneous ribo
210	58.5	8.9	379	2	G82233	phosphoserine amin
211	58.5	8.9	409	2	S41329	5-enolpyruvylshikl
212	58.5	8.9	415	2	T02377	hypothetical prote
213	58.5	8.9	434	2	G83129	probable MFS trans
214	58.5	8.9	469	2	E86421	hypothetical prote
215	58.5	8.9	534	2	F84398	phosphate ABC tran
216	58.5	8.9	591	2	D70562	hypothetical prote
217	58.5	8.9	616	1	RRVOLR	probable RNA-dirc
218	58.5	8.9	627	2	T35608	polyketide hydroxy
219	58.5	8.9	649	2	H86920	probable membrane
220	58.5	8.9	666	2	B56639	1,4-alpha-glucan b
221	58.5	8.9	712	1	YSHUT	threonine-cRNA 11g
222	58.5	8.9	1570	2	AC2012	hypothetical prote
223	58.5	8.9	4302	2	A38971	polycystic kidney
224	58	8.8	112	2	T36440	hypothetical prote
225	58	8.8	140	2	S54242	Ig mu heavy chain
226	58	8.8	221	2	A13631	hypothetical prote
227	58	8.8	247	1	Q08EF1	HXLF3 protein prec
228	58	8.8	270	2	E95034	bifunctional folat
229	58	8.8	272	2	T41070	conserved hypochet
230	58	8.8	278	2	D75585	urase accessory p
231	58	8.8	328	2	T36200	probable DNA polym
232	58	8.8	335	2	F95103	6-phosphotrucokin
233	58	8.8	335	2	D97971	6-phosphotrucokin
234	58	8.8	355	2	B40730	class I histocompa
235	58	8.8	359	2	E83312	hypothetical prote
236	58	8.8	396	2	H87709	HLVD family secret
237	58	8.8	470	1	S78615	argine/threonine/c
238	58	8.8	471	2	S78597	argininosuccinata
239	58	8.8	482	2	B83867	NADP-dependent gly
240	58	8.8	486	2	H83131	5-carboxy-2-hydrox
241	58	8.8	606	2	T31522	WDR1 protein - hum
242	58	8.8	705	2	S54468	Arp1 protein - yea
243	58	8.8	700	2	F64897	hypothetical prote
244	58	8.8	700	2	H85732	probable tons-depe
245	58	8.8	748	2	T37097	hypothetical prote
247	58	8.8	774	2	A28392	probable secreted
248	58	8.8	841	2	S34624	penicillin amidase
						glycogen phosphory

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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:59:53 ; Search time 18 Seconds
(without alignments)
384.454 Million cell updates/sec

Perfect score: 656
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 208217 seqs, 57668156 residues

Total number of hits satisfying chosen parameters: 208217

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Published Applications AA_New:*
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Prsd. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82.5	12.6	602	US-10-449-902-44709	Sequence 44709, A
2	74.5	11.4	160	US-11-056-355B-17946	Sequence 17946, A
3	74	11.3	505	US-10-449-902-38376	Sequence 38376, A
4	72	11.0	426	US-10-449-902-33556	Sequence 33556, A
5	70.5	10.7	419	US-10-953-349-16414	Sequence 16414, A
6	70.5	10.7	449	US-10-449-902-36203	Sequence 36203, A
7	70.5	10.7	456	US-10-953-349-16413	Sequence 16413, A
8	70	10.7	1665	US-11-174-307B-2696	Sequence 2696, Ap
9	69.5	10.6	247	US-11-056-355B-103232	Sequence 103232, A
10	69.5	10.6	247	US-11-056-355B-114471	Sequence 114471, A
11	69.5	10.6	262	US-11-056-355B-103231	Sequence 103231, A
12	69.5	10.6	262	US-11-056-355B-114470	Sequence 114470, A
13	69.5	10.6	995	US-11-174-307B-1572	Sequence 1572, Ap
14	69	10.5	258	US-10-449-902-40020	Sequence 40020, A
15	69	10.5	364	US-11-293-697-3925	Sequence 3925, Ap
16	68.5	10.4	222	US-10-953-349-25727	Sequence 25727, A
17	68.5	10.4	1744	US-11-174-307B-2750	Sequence 2750, Ap
18	68	10.4	512	US-10-449-902-43536	Sequence 43536, A
19	68	10.4	717	US-10-449-902-43536	Sequence 43536, A
20	67.5	10.3	119	US-11-056-355B-420	Sequence 420, App
21	67.5	10.3	180	US-11-293-697-4047	Sequence 4047, Ap
22	67.5	10.3	345	US-10-511-937-2562	Sequence 2562, Ap
23	67	10.2	1079	US-11-174-307B-4958	Sequence 4958, Ap
24	66.5	10.1	1170	US-11-174-307B-1988	Sequence 1988, Ap
25	66	10.1	1907	US-11-174-307B-2770	Sequence 2770, Ap
26	66	10.1	5109	US-11-174-307B-1520	Sequence 1520, Ap

27	65.5	10.0	195	US-11-056-355B-11294	Sequence 11294, A
28	65.5	10.0	255	US-11-056-355B-11293	Sequence 11293, A
29	65.5	10.0	1736	US-11-174-307B-2668	Sequence 2668, Ap
30	65	9.9	178	US-10-953-349-35149	Sequence 35149, A
31	65	9.9	192	US-10-953-349-35148	Sequence 35148, A
32	65	9.9	1257	US-11-174-307B-24	Sequence 24, App1
33	65	9.9	1772	US-11-174-307B-4212	Sequence 4212, Ap
34	64.5	9.8	129	US-10-449-902-42109	Sequence 42109, A
35	64.5	9.8	254	US-11-075-891-6	Sequence 6, App11
36	64.5	9.8	254	US-11-075-891-8	Sequence 8, App11
37	64.5	9.8	254	US-11-075-891-12	Sequence 12, App11
38	64.5	9.8	254	US-11-075-891-14	Sequence 14, App11
39	64.5	9.8	254	US-11-075-891-18	Sequence 18, App11
40	64.5	9.8	254	US-11-075-891-20	Sequence 20, App11
41	64.5	9.8	274	US-11-056-355B-10952	Sequence 10952, A
42	64.5	9.8	282	US-10-953-349-34396	Sequence 34396, A
43	64.5	9.8	520	US-11-056-355B-100323	Sequence 100323, A
44	64.5	9.8	520	US-11-056-355B-111562	Sequence 111562, A
45	64.5	9.8	883	US-11-297-383-11	Sequence 11, App1
46	64.5	9.8	1376	US-11-174-307B-378	Sequence 378, App1
47	64.5	9.8	1379	US-11-174-307B-1738	Sequence 1738, Ap
48	64.5	9.8	1430	US-11-174-307B-982	Sequence 982, App
49	64.5	9.8	3723	US-11-174-307B-2802	Sequence 2802, Ap
50	64	9.8	496	US-10-449-902-54256	Sequence 54256, A
51	64	9.8	793	US-11-056-355B-72585	Sequence 72585, A
52	64	9.8	795	US-11-056-355B-72584	Sequence 72584, A
53	64	9.8	849	US-11-056-355B-72553	Sequence 72553, A
54	64	9.8	1073	US-10-449-902-50549	Sequence 50549, A
55	64	9.8	1933	US-11-174-307B-2226	Sequence 2226, Ap
56	64	9.8	2433	US-11-174-307B-1618	Sequence 1618, Ap
57	63.5	9.7	161	US-10-449-902-46130	Sequence 46130, A
58	63.5	9.7	322	US-11-056-355B-16083	Sequence 16083, A
59	63.5	9.7	349	US-11-056-355B-16082	Sequence 16082, A
60	63.5	9.7	449	US-11-056-355B-36484	Sequence 36484, A
61	63.5	9.7	449	US-11-056-355B-104960	Sequence 104960, A
62	63.5	9.7	449	US-11-056-355B-116199	Sequence 116199, A
63	63.5	9.7	488	US-11-056-355B-16081	Sequence 16081, A
64	63.5	9.7	497	US-10-449-902-65453	Sequence 65453, A
65	63.5	9.7	693	US-10-449-902-69447	Sequence 69447, A
66	63.5	9.7	787	US-10-449-902-51130	Sequence 51130, A
67	63.5	9.7	1773	US-11-174-307B-2658	Sequence 2658, Ap
68	63.5	9.7	1779	US-11-174-307B-2160	Sequence 2160, Ap
69	63.5	9.7	1794	US-11-174-307B-2164	Sequence 2164, Ap
70	63.5	9.7	2498	US-11-174-307B-268	Sequence 268, App
71	63	9.6	233	US-11-289-102-344	Sequence 344, App
72	63	9.6	274	US-10-449-902-40249	Sequence 40249, A
73	63	9.6	319	US-11-056-355B-9046	Sequence 9046, Ap
74	63	9.6	394	US-10-449-902-48126	Sequence 48126, A
75	63	9.6	436	US-10-953-349-18174	Sequence 18174, A
76	63	9.6	483	US-10-449-902-46874	Sequence 46874, A
77	63	9.6	847	US-10-505-928-300	Sequence 300, App
78	63	9.6	1396	US-11-174-307B-466	Sequence 466, App
79	63	9.6	1486	US-11-174-307B-2522	Sequence 2522, Ap
80	63	9.6	1962	US-11-174-307B-1446	Sequence 1446, Ap
81	62.5	9.5	89	US-10-449-902-46974	Sequence 46974, A
82	62.5	9.5	324	US-11-056-355B-15943	Sequence 15943, A
83	62.5	9.5	344	US-10-449-902-23361	Sequence 53361, A
84	62.5	9.5	396	US-11-056-355B-15942	Sequence 15942, A
85	62.5	9.5	436	US-11-056-355B-85631	Sequence 85631, A
86	62.5	9.5	444	US-11-056-355B-85630	Sequence 85630, A
87	62.5	9.5	451	US-11-056-355B-15941	Sequence 15941, A
88	62.5	9.5	467	US-11-056-355B-70389	Sequence 70389, A
89	62.5	9.5	468	US-11-056-355B-70388	Sequence 70388, A
90	62.5	9.5	537	US-11-056-355B-85629	Sequence 85629, A
91	62.5	9.5	561	US-11-174-307B-34	Sequence 34, App1
92	62.5	9.5	561	US-11-056-355B-70387	Sequence 70387, Ap
93	62.5	9.5	1530	US-11-174-307B-1862	Sequence 1862, Ap
94	62.5	9.5	1821	US-11-174-307B-2108	Sequence 2108, Ap
95	62.5	9.5	2110	US-11-174-307B-2010	Sequence 2010, Ap
96	62	9.5	97	US-10-449-902-35058	Sequence 35058, A
97	62	9.5	97	US-10-449-902-48157	Sequence 48157, A
98	62	9.5	102	US-11-301-554-1675	Sequence 1675, Ap
99	62	9.5	180	US-11-056-355B-2889	Sequence 2889, Ap

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101	62	9.5	340	7	US-11-056-355B-6481	Sequence 6481, Ap	174	60	9.1	2368	7	US-11-174-307B-1844	Sequence 2844, Ap
102	62	9.5	373	7	US-11-056-355B-6480	Sequence 6480, Ap	175	60	9.1	2391	7	US-11-174-307B-1386	Sequence 1386, Ap
103	62	9.5	706	7	US-11-056-355B-80144	Sequence 80144, A	176	60	9.1	2574	7	US-11-174-307B-1990	Sequence 1990, Ap
104	62	9.5	720	6	US-10-505-928-383	Sequence 383, App	177	60	9.1	3003	7	US-11-174-307B-228	Sequence 228, App
105	62	9.5	1393	7	US-11-174-307B-606	Sequence 606, App	178	60	9.1	3159	7	US-11-174-307B-1916	Sequence 1916, Ap
106	62	9.5	1471	7	US-11-174-307B-582	Sequence 582, App	179	60	9.1	3362	7	US-11-174-307B-2314	Sequence 2314, Ap
107	62	9.5	1542	7	US-11-174-307B-580	Sequence 50, App1	180	60	9.1	3499	7	US-11-063-438-96	Sequence 96, App1
108	62	9.5	1547	7	US-11-174-307B-1812	Sequence 1212, Ap	181	60	9.1	3512	7	US-11-063-438-83	Sequence 83, App1
109	62	9.5	1929	7	US-11-174-307B-2462	Sequence 2462, Ap	182	60	9.1	3529	7	US-11-063-439-37	Sequence 37, App1
110	62	9.5	2052	7	US-11-174-307B-516	Sequence 516, App	183	60	9.1	3537	7	US-11-063-439-7	Sequence 35, App1
111	61.5	9.4	119	6	US-11-293-697-2647	Sequence 2647, Ap	184	59.5	9.1	120	7	US-11-075-891-35	Sequence 4652, A
112	61.5	9.4	143	6	US-10-449-902-29319	Sequence 29319, A	185	59.5	9.1	131	7	US-11-293-697-4652	Sequence 26974, A
113	61.5	9.4	210	7	US-11-293-697-2698	Sequence 2698, Ap	186	59.5	9.1	126	6	US-10-953-349-8594	Sequence 14634, A
114	61.5	9.4	254	7	US-11-075-891-10	Sequence 10, App1	187	59.5	9.1	240	7	US-11-056-355B-14634	Sequence 31333, A
115	61.5	9.4	254	7	US-11-075-891-16	Sequence 16, App1	188	59.5	9.1	247	6	US-10-449-902-31333	Sequence 14633, A
116	61.5	9.4	254	7	US-11-075-891-22	Sequence 22, App1	189	59.5	9.1	249	7	US-11-056-355B-14633	Sequence 8565, Ap
117	61.5	9.4	323	7	US-11-293-697-4057	Sequence 4057, Ap	190	59.5	9.1	292	7	US-11-056-355B-8565	Sequence 35523, A
118	61.5	9.4	348	6	US-10-449-902-51515	Sequence 51515, A	191	59.5	9.1	301	6	US-11-056-355B-8564	Sequence 31176, A
119	61.5	9.4	348	6	US-10-449-902-56016	Sequence 56016, A	192	59.5	9.1	396	6	US-10-449-902-31176	Sequence 87860, A
120	61.5	9.4	407	6	US-10-449-902-33081	Sequence 33081, A	193	59.5	9.1	453	6	US-10-449-902-31776	Sequence 53670, A
121	61.5	9.4	460	6	US-10-449-902-45508	Sequence 45508, A	194	59.5	9.1	453	6	US-11-056-355B-20257	Sequence 20257, A
122	61.5	9.4	460	6	US-10-449-902-56466	Sequence 56466, A	195	59.5	9.1	470	7	US-11-056-355B-46014	Sequence 46014, A
123	61.5	9.4	1234	6	US-10-449-902-41406	Sequence 41406, A	196	59.5	9.1	587	6	US-10-449-902-45973	Sequence 45973, A
124	61.5	9.4	1298	7	US-11-174-307B-5050	Sequence 3200, Ap	197	59.5	9.1	785	7	US-11-174-307B-1002	Sequence 87860, A
125	61.5	9.4	1574	7	US-11-174-307B-3200	Sequence 1472, Ap	198	59.5	9.1	867	7	US-11-056-355B-87860	Sequence 87859, A
126	61.5	9.4	1610	7	US-11-174-307B-1472	Sequence 2362, Ap	199	59.5	9.1	892	7	US-11-056-355B-87859	Sequence 87858, A
127	61.5	9.4	1925	7	US-11-174-307B-2362	Sequence 2012, Ap	200	59.5	9.1	916	7	US-11-056-355B-87858	Sequence 45211, A
128	61.5	9.4	2269	7	US-11-174-307B-2012	Sequence 2660, Ap	201	59.5	9.1	935	7	US-11-056-355B-45210	Sequence 45270, A
129	61.5	9.4	2416	7	US-11-174-307B-4660	Sequence 103, App	202	59.5	9.1	959	7	US-11-056-355B-45270	Sequence 45269, A
130	61.5	9.4	3493	7	US-11-063-439-103	Sequence 102, App	203	59.5	9.1	998	7	US-11-056-355B-45269	Sequence 1632, Ap
131	61.5	9.4	3497	7	US-11-063-439-102	Sequence 2734, Ap	204	59.5	9.1	1215	7	US-11-174-307B-1632	Sequence 1210, Ap
132	61	9.3	247	7	US-11-293-697-2734	Sequence 56481, A	205	59.5	9.1	1324	7	US-11-174-307B-1210	Sequence 474, App
133	61	9.3	439	6	US-10-449-902-35737	Sequence 588, App	206	59.5	9.1	1374	7	US-11-174-307B-474	Sequence 2556, Ap
134	61	9.3	868	6	US-10-449-902-56481	Sequence 588, App	207	59.5	9.1	1463	7	US-11-174-307B-2526	Sequence 5194, Ap
135	61	9.3	1316	7	US-11-174-307B-588	Sequence 2278, Ap	208	59.5	9.1	1766	7	US-11-174-307B-5194	Sequence 2884, Ap
136	61	9.3	1355	7	US-11-174-307B-2278	Sequence 1346, Ap	209	59.5	9.1	1897	7	US-11-174-307B-2884	Sequence 920, App
137	61	9.3	1606	7	US-11-174-307B-4978	Sequence 3214, Ap	210	59.5	9.1	2228	7	US-11-174-307B-920	Sequence 2292, Ap
138	61	9.3	1880	7	US-11-174-307B-1346	Sequence 1488, Ap	211	59.5	9.1	4709	7	US-11-174-307B-2292	Sequence 46613, A
139	61	9.3	2149	7	US-11-174-307B-3214	Sequence 33, App1	212	59	9.0	88	6	US-10-953-349-46013	Sequence 26061, A
140	61	9.3	2598	7	US-11-174-307B-1488	Sequence 8196, App1	213	59	9.0	120	6	US-10-953-349-46013	Sequence 3751, App
141	60.5	9.2	120	7	US-11-075-891-33	Sequence 33, App1	214	59	9.0	126	7	US-11-056-355B-3751	Sequence 393, App
142	60.5	9.2	120	7	US-11-075-891-34	Sequence 8196, App	215	59	9.0	225	7	US-11-197-712-393	Sequence 71601, A
143	60.5	9.2	352	7	US-11-056-355B-8196	Sequence 19, App1	216	59	9.0	230	7	US-11-056-355B-18191	Sequence 3533, Ap
144	60.5	9.2	507	7	US-11-296-657-19	Sequence 4104, Ap	217	59	9.0	261	7	US-11-293-657-513	Sequence 71600, A
145	60.5	9.2	578	7	US-11-174-307B-4104	Sequence 4500, Ap	218	59	9.0	318	7	US-11-056-355B-71800	Sequence 47624, A
146	60.5	9.2	689	7	US-11-174-307B-4500	Sequence 1648, Ap	219	59	9.0	319	6	US-10-449-902-47624	Sequence 38750, A
147	60.5	9.2	728	6	US-10-504-973-10	Sequence 4996, Ap	220	59	9.0	418	7	US-11-056-355B-71799	Sequence 3088, Ap
148	60.5	9.2	1501	7	US-11-174-307B-1648	Sequence 104, App	221	59	9.0	795	7	US-11-174-307B-2434	Sequence 1856, Ap
149	60.5	9.2	1628	7	US-11-174-307B-2748	Sequence 36487, A	222	59	9.0	983	7	US-11-174-307B-1856	Sequence 226, App
150	60.5	9.2	2088	7	US-11-174-307B-4996	Sequence 37359, A	223	59	9.0	987	7	US-11-174-307B-236	Sequence 1432, App
151	60.5	9.2	3460	6	US-10-505-928-104	Sequence 36487, A	224	59	9.0	999	7	US-11-174-307B-1422	Sequence 1366, Ap
152	60	9.1	91	6	US-10-449-902-36487	Sequence 3870, Ap	225	59	9.0	1066	7	US-11-174-307B-1396	Sequence 2006, Ap
153	60	9.1	308	6	US-11-293-697-3870	Sequence 47271, A	226	59	9.0	1098	7	US-11-174-307B-2006	Sequence 1458, Ap
154	60	9.1	485	6	US-10-449-902-37359	Sequence 41529, A	227	59	9.0	1117	7	US-11-174-307B-1458	Sequence 2314, Ap
155	60	9.1	574	6	US-10-449-902-36659	Sequence 500, App	228	59	9.0	1148	7	US-11-247-437-6	Sequence 3718, App1
156	60	9.1	713	6	US-11-056-355B-47272	Sequence 500, App	229	59	9.0	1452	7	US-11-174-307B-4154	Sequence 4154, Ap
157	60	9.1	716	7	US-11-056-355B-47271	Sequence 1300, App	230	59	9.0	1592	7	US-11-174-307B-5088	Sequence 5088, Ap
158	60	9.1	752	7	US-11-056-355B-47270	Sequence 1300, App	231	59	9.0	1596	7	US-11-174-307B-792	Sequence 792, App
159	60	9.1	1006	6	US-10-449-902-41503	Sequence 41328, A	232	59	9.0	1937	7	US-11-174-307B-3074	Sequence 3074, Ap
160	60	9.1	1039	6	US-10-449-902-41129	Sequence 2154, Ap	233	59	9.0	1962	7	US-11-174-307B-1748	Sequence 1748, Ap
161	60	9.1	1153	7	US-11-174-307B-500	Sequence 2516, Ap	234	59	9.0	2101	7	US-11-174-307B-2754	Sequence 2754, Ap
162	60	9.1	1170	7	US-11-174-307B-1300	Sequence 2208, Ap	235	59	9.0	2494	7	US-11-063-439-50	Sequence 778, App
163	60	9.1	1187	7	US-11-174-307B-1728	Sequence 2208, Ap	236	59	9.0	3494	7	US-11-063-439-50	Sequence 53, App1
164	60	9.1	1310	6	US-10-449-902-41328	Sequence 1770, Ap	237	59	9.0	3503	7	US-11-063-439-53	Sequence 72, App1
165	60	9.1	1369	7	US-11-174-307B-2154	Sequence 2190, Ap	238	59	9.0	3512	7	US-11-063-439-72	Sequence 18425, A
166	60	9.1	1370	7	US-11-174-307B-2490	Sequence 1198, App	239	59	9.0	3512	7	US-11-063-439-72	Sequence 18425, A
167	60	9.1	1420	7	US-11-174-307B-2516	Sequence 1198, App	240	59	9.0	3512	7	US-11-063-439-72	Sequence 18425, A
168	60	9.1	1566	7	US-11-174-307B-2208	Sequence 1198, App	241	59	9.0	3512	7	US-11-063-439-72	Sequence 18425, A
169	60	9.1	1614	7	US-11-174-307B-1770	Sequence 1198, App	242	59	9.0	3512	7	US-11-063-439-72	Sequence 18425, A
170	60	9.1	1673	7	US-11-174-307B-1178	Sequence 1198, App	243	59	9.0	3512	7	US-11-063-439-72	Sequence 18425, A
171	60	9.1	1711	7	US-11-174-307B-2190	Sequence 1198, App	244	59	9.0	3512	7	US-11-063-439-72	Sequence 18425, A
172	60	9.1	1753	7	US-11-174-307B-1198	Sequence 1198, App	245	58.5	8.9	202	7	US-11-056-355B-18424	Sequence 18424, A

OM protein - protein search, using sw model
Run on: July 20, 2006, 09:50:42 ; Search time 83 Seconds
(without alignments)
661.036 Million cell updates/sec

Title: US-09-997-585-399
Perfect score: 656
Sequence: 1 MLPALPALVFTVMSLLA.....SAQLLCMPVGVARGALCQ 120
Scoring table: BLOSUM62
Gapop 10 0, Gapext 0 5
2589679 segs, 457216429 residues
Total number of hits satisfying chosen parameters: 2589679
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database :
A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAY66754	standard;	protein;	120	AA.	
DE	Membrane-bound protein PRO1187.					
PN	WO963088-A2.					
PD	09-DEC-1999.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 656;	DB 3;	Length 120;	
Best Local Similarity		100.0%;	Pred. No. 1.7e-67;			
RESULT 2						
ID	AAB24077	standard;	protein;	120	AA.	
DE	Human PRO1187 protein sequence SEQ ID NO:55.					
PN	WO200053755-A2.					
PD	14-SEP-2000.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 656;	DB 3;	Length 120;	
Best Local Similarity		100.0%;	Pred. No. 1.7e-67;			
RESULT 3						
ID	AAB65277	standard;	protein;	120	AA.	
DE	Human PRO1187 (UNQ601) protein sequence SEQ ID NO:399.					
PN	WO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 656;	DB 4;	Length 120;	
Best Local Similarity		100.0%;	Pred. No. 1.7e-67;			
RESULT 4						
ID	ABP69105	standard;	protein;	120	AA.	
DE	Human polypeptide SEQ ID NO 1152.					
PN	WO200270539-A2.					
PD	12-SEP-2002.					
PA	(HYSE-) HYSEQ INC.					
Query Match		100.0%;	Score 656;	DB 5;	Length 120;	
Best Local Similarity		100.0%;	Pred. No. 1.7e-67;			
RESULT 5						
ID	AAU83640	standard;	protein;	120	AA.	
DE	Human PRO protein, Seq ID No 98.					
PN	WO200208288-A2.					
PD	31-JAN-2002.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 656;	DB 5;	Length 120;	
Best Local Similarity		100.0%;	Pred. No. 1.7e-67;			
RESULT 6						
ID	ADY31838	standard;	protein;	120	AA.	
DE	Novel human secreted and transmembrane protein PRO1187.					

PN	WO200193983-A1.					
PD	13-DEC-2001.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 656;	DB 5;	Length 120;	
Best Local Similarity		100.0%;	Pred. No. 1.7e-67;			
RESULT 7						
ID	ABU58092	standard;	protein;	120	AA.	
DE	Human PRO polypeptide #124.					
PN	US2003027163-A1.					
PD	06-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 656;	DB 6;	Length 120;	
Best Local Similarity		100.0%;	Pred. No. 1.7e-67;			
RESULT 8						
ID	ABU59170	standard;	protein;	120	AA.	
DE	Novel human secreted or transmembrane protein PRO1187.					
PN	US2002132252-A1.					
PD	19-SEP-2002.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 656;	DB 6;	Length 120;	
Best Local Similarity		100.0%;	Pred. No. 1.7e-67;			
RESULT 9						
ID	ABU82682	standard;	protein;	120	AA.	
DE	Human secreted/transmembrane protein PRO1187.					
PN	US2003032023-A1.					
PD	13-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 656;	DB 6;	Length 120;	
Best Local Similarity		100.0%;	Pred. No. 1.7e-67;			
RESULT 10						
ID	ABU60601	standard;	protein;	120	AA.	
DE	Human secreted/transmembrane protein, #160.					
PN	US2002160384-A1.					
PD	31-OCT-2002.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 656;	DB 6;	Length 120;	
Best Local Similarity		100.0%;	Pred. No. 1.7e-67;			
RESULT 11						
ID	ABU80787	standard;	protein;	120	AA.	
DE	Human PRO polypeptide #49.					
PN	US2003036635-A1.					
PD	20-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 656;	DB 6;	Length 120;	
Best Local Similarity		100.0%;	Pred. No. 1.7e-67;			
RESULT 12						
ID	ABO33753	standard;	protein;	120	AA.	
DE	Novel human secreted and transmembrane protein PRO1187.					
PN	US2003045687-A1.					
PD	06-MAR-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 656;	DB 6;	Length 120;	
Best Local Similarity		100.0%;	Pred. No. 1.7e-67;			
RESULT 13						
ID	ABU13983	standard;	protein;	120	AA.	
DE	Human PRO1187 polypeptide.					
PN	US2002103125-A1.					
PD	01-AUG-2002.					
PA	(GETH) GENENTECH LTD.					
Query Match		100.0%;	Score 656;	DB 6;	Length 120;	
Best Local Similarity		100.0%;	Pred. No. 1.7e-67;			
RESULT 14						
ID	ABU72568	standard;	protein;	120	AA.	
DE	Novel human secreted and transmembrane protein PRO1187.					
PN	US2003003531-A1.					
PD	02-JAN-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 656;	DB 6;	Length 120;	
Best Local Similarity		100.0%;	Pred. No. 1.7e-67;			
RESULT 15						
ID	ABU59317	standard;	protein;	120	AA.	
DE	Human secreted/transmembrane protein, #160.					
PN	US2003027162-A1.					
PD	06-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 656;	DB 6;	Length 120;	

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Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 16
ID ABO26014 standard; protein; 120 AA.
DE Human PRO1187 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 17
ID ABU82096 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1187.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 18
ID ABUS9023 standard; protein; 120 AA.
DE Human secreted/transmembrane protein, #160.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 19
ID ABUS2401 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1187.
PN US2003022187-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 20
ID ABUS9466 standard; protein; 120 AA.
DE Novel human secreted or transmembrane protein PRO1185.
PN US2003027985-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 21
ID ABUS2232 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1187.
PN US2003017476-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 22
ID ABUI0938 standard; protein; 120 AA.
DE Human PRO polypeptide #124.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 23
ID ABUS1690 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1187.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 24
ID ABUS8629 standard; protein; 120 AA.
DE Human secreted and transmembrane polypeptide PRO1187.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 25
ID ABO34143 standard; protein; 120 AA.
DE Human PRO1187 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 26
ID ABJ72276 standard; protein; 120 AA.
DE Human PRO1187 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 27
ID ADA37910 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1187.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 28
ID ADA21596 standard; protein; 120 AA.
DE Human secreted/transmembrane polypeptide PRO1187.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 29
ID ADA10383 standard; protein; 120 AA.
DE Human secreted/transmembrane protein, PRO1187.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 30
ID ADA17927 standard; protein; 120 AA.
DE Human PRO1187 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 31
ID ADA28035 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1187.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 32
ID ADA94615 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1187.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 33
ID ADA38840 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1187.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 34
ID ABJ72404 standard; protein; 120 AA.
DE Human PRO1187 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 656; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
RESULT 35
ID ADA2961 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1187.
```


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OM protein - protein search, using sw model

Run on: July 20, 2006, 09:54:22 ; Search time 140 Seconds

(without alignments)
792.871 Million cell updates/sec

Title: US-09-997-585-399

Perfect score: 656
Sequence: 1 MLPPALPPALVFTVAMSLA.....SAQLLCMPVGARGALNQ 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Uniprot 7.2:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	656	100.0	120	2	Q6UM09 HUMAN
2	85	13.0	638	2	Q3SID4 THIDA
3	83	12.7	502	2	Q9X8T8 STRCO
4	82.5	12.6	602	2	Q5JLX7 ORYSA
5	82.5	12.6	733	2	Q8L1Z0 ORYSA
6	82	12.5	741	2	Q2JDC2 GACTO
7	81.5	12.4	848	2	Q46T89 RALFJ
8	80.5	12.3	371	2	Q73YK5 MYCPA
9	79.5	12.1	443	2	Q8D981 VIBVU
10	78.5	12.0	476	2	Q7ML91 VIBVY
11	78	11.9	156	2	Q5ZAG4 ORYSA
12	77.5	11.8	126	2	Q8LMB7 ORYSA
13	77.5	11.8	153	2	Q339N8 ORYSA
14	77.5	11.8	246	2	Q6NKA1 CORDI
15	77.5	11.8	432	1	V1S10 MYCTU
16	77.5	11.8	737	2	Q80ZM8 BRARP
17	77	11.7	229	2	Q3JK00 BURPI
18	77	11.7	294	2	Q96440 LEICH
19	77	11.7	477	2	Q6NCK7 RHOPA
20	76.5	11.7	170	2	Q8M6E8 SCAND
21	76.5	11.7	195	2	Q2UTB6 SCYAN
22	76.5	11.7	259	2	Q6ZRH4 HUMAN
23	76	11.6	156	2	Q4ME72 ASPBU
24	76	11.6	379	2	Q4AQ24 9BURK
25	76	11.6	1133	1	SRBP1 CRIGR
26	75.5	11.5	258	2	Q74MK0 NANEQ
27	75.5	11.5	368	1	ILVE MYCTB
28	75.5	11.5	371	2	Q6NG91 CORDI
29	75	11.4	432	2	Q5P855 AZOSE
30	75	11.4	829	2	Q3FXU8 9DELT
31	75	11.4	927	2	Q2RPM4 RHORU

32	74.5	11.4	175	2	Q5X2P1 LEGPA	05x2p1 legionella
33	74.5	11.4	372	2	Q60B43 METCA	Q6b43 methylococc
34	74.5	11.4	835	1	B6AL LYCES	P46980 lycopersico
35	74.5	11.4	835	2	Q546T5 LYCES	Q546t5 lycopersico
36	74	11.3	176	2	Q5QK27 ANAPH	Q5qk27 anaplama p
37	74	11.3	317	2	Q7SP99 NEUCR	Q7sp99 neurospora
38	74	11.3	539	2	Q5NSN0 CRYNE	Q5nsn0 cryptococcu
39	74	11.3	790	2	Q94GL4 ORYSA	Q94gl4 oryza sativ
40	74	11.3	804	2	Q82RI6 STRAM	Q82ri6 streptomyc
41	74	11.3	2192	2	Q74F55 GEOSL	Q74f55 geobacter s
42	73.5	11.2	110	2	Q4CL01 TRYCR	Q4cl01 trypanosoma
43	73.5	11.2	381	2	Q3LZK8 9CAUD	Q3lzk8 acrythosiph
44	73.5	11.2	390	2	Q9TIR0 BPAPS	Q9tir0 bacterioph
45	73.5	11.2	433	2	Q7MEP5 VIBVU	Q7mef5 vibrio vuln
46	73.5	11.2	433	2	Q6DTB6 VIBVU	Q6dtb6 vibrio vuln
47	73.5	11.2	440	2	Q7PTM3 ANOGA	Q7ptm3 anophelis g
48	73.5	11.2	854	2	Q47PE0 THEFY	Q47pe0 thermobifid
49	73.5	11.2	3649	2	Q83WE8 MITCR	Q83we8 micromonop
50	73.5	11.2	136	2	Q99QA4 STRCO	Q99qa4 streptomyce
51	73	11.1	166	2	Q2RBD3 ORYSA	Q2rbd3 oryza sativ
52	73	11.1	202	2	Q3R2H1 XYLFA	Q3r2h1 xyella las
53	73	11.1	224	2	Q8U9E7 AGRTS	Q8u9e7 agrobacteri
54	73	11.1	229	2	Q62B14 BURMA	Q62b14 burkholderi
55	73	11.1	229	2	Q63J63 BURPS	Q63j63 burkholderi
56	73	11.1	229	2	Q8PK02 XANAC	Q8pk02 xanthomonas
57	73	11.1	244	2	Q7CTA5 AGRTS	Q7cta5 agrobacteri
58	72.5	11.1	325	2	Q7V8J5 PROMM	Q7v8j5 prochloroco
59	72.5	11.1	339	2	Q8B1E5 MOUSE	Q8b1e5 mus musculu
60	72.5	11.1	355	2	Q32JL4 SHIDS	Q32jl4 shigella dy
61	72.5	11.1	359	2	Q985C2 RHILLO	Q985c2 rhizobium l
62	72.5	11.1	378	2	Q7UNU2 RHOPA	Q7unu2 rhodospirill
63	72.5	11.1	477	2	Q88N51 PSEPK	Q88n51 pseudomonas
64	72.5	11.1	3104	2	Q04846 CORAM	Q04846 corynebacte
65	72	11.0	159	2	Q9H233 PSEBAE	Q9h233 pseudomonas
66	72	11.0	247	2	Q3BSC0 XANCS	Q3bse0 xanthomonas
67	72	11.0	386	2	Q981X7 RHILLO	Q981x7 rhizobium l
68	72	11.0	426	2	Q5N7M4 ORYSA	Q5n7m4 oryza sativ
69	72	11.0	540	2	Q5KC55 CRVNE	Q5kc55 cryptococcu
70	72	11.0	1063	1	SPTS YEAST	P27692 saccharomyc
71	71.5	10.9	144	2	Q4T1R8 YETNG	Q4t1r8 tetradodon n
72	71.5	10.9	175	2	Q5ZM01 LEGPH	Q5zmq1 legionella
73	71.5	10.9	236	2	Q924Z1 STRCO	Q924z1 streptomyce
74	71.5	10.9	267	2	Q3X2M5 9ACTN	Q3x2m5 rhizobacter
75	71.5	10.9	272	2	Q8XRN3 RALSO	Q8xrn3 ralsonia s
76	71.5	10.9	418	2	Q43781 LOTYA	Q43781 lotus japon
77	71.5	10.9	77	2	Q3SWY0 9GAMM	Q3swy0 shewanella
78	71.5	10.9	1128	2	Q5F488 CHICK	Q5f488 gallus galli
79	71	10.8	210	2	Q9RVL7 DEIRA	Q9rvl7 deinococcus
80	71	10.8	229	2	Q2TXV7 BURTH	Q2txv7 burkholderi
81	71	10.8	266	2	Q6C6U2 YARLI	Q6c6u2 yarrowia li
82	71	10.8	268	2	Q4S483 YETNG	Q4s483 tetradodon n
83	71	10.8	275	2	Q2XNL5 CHICK	Q2xnl5 gallus galli
84	71	10.8	283	1	Y393 IDILO	Q5r012 idiomarina
85	71	10.8	303	2	Q3FMD6 9BURK	Q3fme6 rhodoferrax
86	71	10.8	321	2	Q57G10 SALCH	Q57g10 salmonella
87	71	10.8	321	2	Q8ZK75 SALTY	Q8zkr5 salmonella
88	71	10.8	342	2	Q8ZCW5 YERPE	Q8zcy5 yersinia pe
89	71	10.8	351	2	Q4MCG6 ASPBU	Q4mcb6 aspergillus
90	71	10.8	405	2	Q2QSG8 ORYSA	Q2qsg8 oryza sativ
91	71	10.8	419	2	Q84NY5 ORYSA	Q84ny5 oryza sativ
92	71	10.8	450	2	Q7ZTX1 TRIYI	Q7ztx1 trichoderma
93	71	10.8	529	2	Q37TL0 SPHAR	Q37tl0 novosphingo
94	71	10.8	608	2	Q8K2I9 PSEBU	Q8k2i9 pseudomonas
95	71	10.8	766	2	Q2RON5 ORYSA	Q2ron5 oryza sativ
96	71	10.8	4311	2	Q7YOK5 CANPA	Q7yok5 canis famli
97	70.5	10.7	151	2	Q44BV3 CHRSL	Q44bv3 chromohalob
98	70.5	10.7	227	2	Q93783 HUMGT	Q93783 humicola gr
99	70.5	10.7	243	2	Q8PMI7 XANAC	Q8pmi7 xanthomonas
100	70.5	10.7	291	2	Q5GYS7 XANOR	Q5gys7 xanthomonas
101	70.5	10.7	368	1	ILVE MYCTU	Q5gys7 xanthomonas
102	70.5	10.7	368	2	Q7TYX3 MYCBO	Q7tyx3 mycobacteri
103	70.5	10.7	370	2	Q80V44 MOUSE	Q80v44 mus musculu
104	70.5	10.7	410	2	Q4KX26_PSEBS	Q4kb26 pseudomonas

105	70.5	10.7	418	2	02XIP7_PSEBU	02XIP7_pseudomonas	178	69	10.5	940	2	04WJP5_ASFPV	04WJP5_aspergillus
106	70.5	10.7	418	2	088TK5_PSEBK	088TK5_pseudomonas	179	69	10.5	1024	2	SRBP1_RAT	P56720 rattus norv
107	70.5	10.7	419	2	07GIG6_SOYBN	07GIG6_glycine max	180	69	10.5	1134	1	SRBP1_MOUSE	096720 mus musculus
108	70.5	10.7	420	2	040107_LUPAN	040107_lupinus ang	181	69	10.5	1173	2	03TGI0_RHOA	037910 rhodopseudo
109	70.5	10.7	420	2	040108_LUPAN	040108_lupinus ang	182	69	10.5	1234	2	09HPM2_HALISA	09HPM2_haibacteri
110	70.5	10.7	411	2	07NJY7_GLOVI	07NJY7_gloeobacter	183	69	10.5	1501	2	06JMR3_BURP1	06JMR3_burholderi
111	70.5	10.7	466	2	048548_SOYBN	048548_glycine max	184	69	10.5	1511	2	03JGK2_BURP1	03JGK2_burholderi
112	70.5	10.7	477	2	03UDP5_MOUSE	03UDP5_mus musculus	185	1607	10.5	1607	2	07OHZ9_PACTO	07OHZ9_streptomyce
113	70.5	10.7	513	2	046334_9BUDK	046334_comamonas	186	69	10.5	1960	2	064HK6_PACTO	064HK6_streptomyce
114	70.5	10.7	521	2	03TOP5_MOUSE	03TOP5_mus musculus	187	69	10.5	2184	2	04P5Y6_USTMA	04P5Y6_ustilago ma
115	70.5	10.7	535	2	06EUP2_ORYSA	06EUP2_oryza sativ	188	69	10.5	3500	2	07O100_PACTO	07O100_pactomyce
116	70.5	10.7	559	2	03TTR4_PSEAE	03TTR4_oryza sativ	189	68.5	10.4	189	2	07ULY6_RHOBA	07ULY6_rhodopirell
117	70.5	10.7	591	2	0913V3_PSEAE	0913V3_pseudomonas	190	68.5	10.4	281	2	07NT57_CHRVO	07NT57_chromobacte
118	70.5	10.7	684	2	03EC98_9BRAD	03EC98_bradycrizob	191	68.5	10.4	291	2	021XJ3_RHOA	021XJ3_rhodopseudo
119	70.5	10.7	728	2	05RKS5_PONPY	05RKS5_pongo pygma	192	68.5	10.4	306	2	05IGM8_9CAUD	05IGM8_bacterioph
120	70.5	10.7	777	2	06PAS9_MOUSE	06PAS9_mus musculus	193	68.5	10.4	464	2	06XMY6_RHOER	06XMY6_rhodococcus
121	70.5	10.7	1005	2	03TEB3_MOUSE	03TEB3_mus musculus	194	68.5	10.4	502	2	04P717_USTMA	04P717_ustilago ma
122	70.5	10.7	1005	2	08BLR5_MOUSE	08BLR5_m 10 days n	195	68.5	10.4	513	2	024715_COWTE	024715_comamonas t
123	70.5	10.7	1046	2	038119_9TRYR	038119_trypanosoma	196	68.5	10.4	551	2	09BN27_RHIL0	09BN27_rhizobium 1
124	70.5	10.7	1441	2	08ORP2_MOUSE	08ORP2_mus musculus	197	68.5	10.4	610	2	02TXM7_ASFOR	02TXM7_aspergillus
125	70.5	10.7	2038	2	05PRF0_MOUSE	05PRF0_mus musculus	198	68.5	10.4	748	2	02OVNO_ORYSA	02OVNO_oryza sativ
126	70	10.7	206	2	08ZSQ6_PYRAE	08ZSQ6_pyrobaculum	199	68.5	10.4	748	2	08ECT4_SHEON	08ECT4_shewanella
127	70	10.7	321	2	05PJ70_SALPA	05PJ70_salmonella	200	68.5	10.4	931	2	04KAL5_PSEF5	04KAL5_pseudomonas
128	70	10.7	321	2	08Z156_SALPA	08Z156_salmonella	201	68.5	10.4	1106	2	04FY01_LEIMA	04FY01_leishmania
129	70	10.7	416	2	07XGV9_ORYSA	07XGV9_oryza sativ	202	68	10.4	230	2	04IG74_GIBZE	04IG74_gibberella
130	70	10.7	416	2	094HT1_ORYSA	094HT1_oryza sativ	203	68	10.4	381	2	0855F3_9CAUD	0855F3_mycobacteri
131	70	10.7	445	2	04NKG7_9MTCB	04NKG7_athrobacte	204	68	10.4	378	2	03HVB2_XANCS	03HVB2_xanthomonas
132	70	10.7	445	2	03QSA0_9RHOB	03QSA0_silicibacte	205	68	10.4	409	2	04S920_TETNG	04S920_tetradon n
133	70	10.7	478	2	09A9Y9_CAUCR	09A9Y9_caulobacter	206	68	10.4	432	2	04JON7_SOLUS	04JON7_bolibacter
134	70	10.7	537	2	02J561_PACTO	02J561_fraklia sp.	207	68	10.4	524	2	PURAI_CHRVO	07P071_chromobacte
135	70	10.7	598	1	PANK1_HUMAN	08TE04_homo sapien	208	68	10.4	581	1	04CYE1_TRYCR	04CYE1_borrelia bu
136	70	10.7	778	2	05BAM2_EMENT	05BAM2_aspergillus	209	68	10.4	581	1	SYR_BORBU	053138 mycobacteri
137	70	10.7	949	2	04TKZ5_THERY	04TKZ5_thermobifid	210	68	10.4	592	2	07VEM4_MYCTU	07VEM4_mycobacteri
138	70	10.7	1646	2	07WTE3_PACTO	07WTE3_streptomyce	211	68	10.4	663	2	03TVYX1_MOUSE	03TVYX1_mus musculus
139	69.5	10.6	154	2	02UTB4_ASFOR	02UTB4_aspergillus	212	68	10.4	697	2	03BU52_XANCS	03BU52_xanthomonas
140	69.5	10.6	220	2	069L96_ORYSA	069L96_oryza sativ	213	68	10.4	697	2	08PL70_XANAC	08PL70_xanthomonas
141	69.5	10.6	220	2	08KFX6_CHLTE	08KFX6_chlorobium	214	68	10.4	717	2	07XOR8_ORYSA	07XOR8_oryza sativ
142	69.5	10.6	224	2	06H8H2_ORYSA	06H8H2_oryza sativ	215	68	10.4	717	2	0502N3_BRARE	0502N3_birchydantio
143	69.5	10.6	247	2	084T14_ARATH	084T14_arabidopsis	216	68	10.4	866	2	099UK7_MOUSE	099UK7_mus musculus
144	69.5	10.6	247	2	091LN6_ARATH	091LN6_arabidopsis	217	68	10.4	1022	2	05SRX5_MOUSE	05SRX5_mus musculus
145	69.5	10.6	345	1	YKCO_CABEL	P42001_caenorhabdi	218	68	10.4	1069	2	03U4S8_MOUSE	03U4S8_mus musculus
146	69.5	10.6	345	2	09X7U8_STRCO	09X7U8_streptomyce	219	68	10.4	1075	2	056RX6_MOUSE	056RX6_mus musculus
147	69.5	10.6	380	2	08ZNO5_STRAM	08ZNO5_streptomyce	220	68	10.4	1078	2	07NMW9_CHRVO	07NMW9_chromobacte
148	69.5	10.6	418	1	AAAT1_MEDSA	P28011_medicago sa	221	68	10.4	1134	2	03UDJ3_MOUSE	03UDJ3_mus musculus
149	69.5	10.6	535	1	YB97_MYCTU	P64751_mycobacteri	222	68	10.4	1134	2	08CT73_MOUSE	08CT73_m 0 day neo
150	69.5	10.6	535	1	Y921_MYCBO	P64752_mycobacteri	223	68	10.4	1240	2	04QOV2_LEIMA	04QOV2_leishmania
151	69.5	10.6	738	1	PIOD3_HUMAN	05R658_homo sapien	224	68	10.4	1384	1	CNTP1_HUMAN	P78157_homo sapien
152	69.5	10.6	857	2	PIOD3_PONPY	05R6K5_pongo pygma	225	68	10.4	2024	2	09EWA3_PACTO	09EWA3_streptomyce
153	69.5	10.6	857	2	03GVH5_PACTO	03GVH5_nocardioide	226	68	10.4	2302	2	06OWM3_CABER	06OWM3_caenorhabdi
154	69.5	10.6	908	2	05B337_EMENT	05B337_aspergillus	227	68	10.3	2430	2	0303P5_SRRSU	0303P5_streptococc
155	69	10.5	121	2	07RTG6_MOUSE	07RTG6_m 4 days ne	228	67.5	10.3	91	2	0447F5_SOLUS	0447F5_solibacter
156	69	10.5	160	2	07W7X3_BORPA	07W7X3_bordetella	229	67.5	10.3	206	2	045VU9_PABPO	045VU9_praenibacill
157	69	10.5	178	2	07WLB3_BORBR	07WLB3_oryza sativ	230	67.5	10.3	211	2	06Z8O7_ORYSA	06Z8O7_oryza sativ
158	69	10.5	160	2	06ES44_ORYSA	06ES44_oryza sativ	231	67.5	10.3	227	2	031LV8_SYNP7	031LV8_synp7
159	69	10.5	229	2	02P2C6_XANOR	02P2C6_xanthomonas	232	67.5	10.3	256	2	05N017_SYNP6	05N017_synp6
160	69	10.5	229	2	05GZB7_XANOR	05GZB7_xanthomonas	233	67.5	10.3	345	2	09RU00_DEIRA	09RU00_delmococcus
161	69	10.5	262	2	034Y69_9GAMM	034Y69_alkalilimna	234	67.5	10.3	312	2	09WZ54_HUMAN	09WZ54_homo sapien
162	69	10.5	319	2	08RIH2_MOUSE	08RIH2_mus musculus	235	67.5	10.3	361	2	06X3X7_IPOPU	06X3X7_ipomoea pur
163	69	10.5	342	2	0668D1_YERPS	0668D1_yersinia ps	236	67.5	10.3	361	2	06X3X8_IPONI	06X3X8_ipomoea nll
164	69	10.5	348	2	04SEN8_TETNG	04SEN8_tetradon n	237	67.5	10.3	361	2	06X3Y0_IPOHE	06X3Y0_ipomoea hed
165	69	10.5	381	2	03XT41_9PROT	03XT41_magnetococc	238	67.5	10.3	361	2	06X3Y0_IPOHE	06X3Y0_ipomoea hed
166	69	10.5	416	2	03WMH2_9RHIZ	03WMH2_mesorhizobi	239	67.5	10.3	369	2	006055_MYCGO	006055_mycobacteri
167	69	10.5	466	2	093785_TRIIE	093785_trichoderma	240	67.5	10.3	389	2	03AV73_SYNS9	03AV73_syns9
168	69	10.5	466	2	066PP5_FRIAN	066PP5_fragaria an	241	67.5	10.3	391	2	04JYMD5_CORJX	04JYMD5_corynebacte
169	69	10.5	468	2	P96444_RHIME	P96444_rhizobium m	242	67.5	10.3	405	2	08RY22_STRCO	08RY22_streptomyce
170	69	10.5	484	2	04DKE8_TRYCR	04DKE8_trypanosoma	243	67.5	10.3	420	2	022603_IPOPU	022603_ipomoea pur
171	69	10.5	546	2	08CJN9_STRCO	08CJN9_streptomyce	244	67.5	10.3	452	2	04WR02_ASFPV	04WR02_aspergillus
172	69	10.5	547	2	03AIM3_SYNSC	03AIM3_synschoce	245	67.5	10.3	477	2	02X8E3_PSEBU	02X8E3_pseudomonas
173	69	10.5	705	2	096B28_HUMAN	096B28_homo sapien	246	67.5	10.3	490	2	033TR7_9GAMM	033TR7_shewanella
174	69	10.5	709	2	05XFT1_BRARE	05XFT1_brachydantio	247	67.5	10.3	527	2	09PUH8_ARATH	09PUH8_arabidopsis
175	69	10.5	729	2	090ZN6_BRARE	090ZN6_brachydantio	248	67.5	10.3	658	2	05ARI8_EMENT	05ARI8_aspergillus
176	69	10.5	893	2	03HYA0_PSEBD	03HYA0_pseudomonas	249	67.5	10.3	674	2	07OKC1_PACTO	07OKC1_gordonia we
177	69	10.5	893	2	092V32_RHIME	092V32_rhizobium m	250	67.5	10.3	674	2		